

BLASTP 2.2.1 [Apr-13-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Singhui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nuclei: Acids Res. 25:3389-3402.

RID: 1003946835-11327-26633

Query=

(10 letters) CATDIKGAEC) CNOWLAY

Database: nr

777,663 sequences; 247,121,334 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Sequences producing significant alignments:	tid)	s) Valu
gi:9154.2:gb.AAA72:92.1: (030393) T-cell receptor alpha V-J gi:1433 434(emb):7A 940813.1) - (AJ:14790 putative zinc finger gi 43. (33);gb(AAD10406.1) - (AF:01053 - Suter surface protein		181 306 336
WILLIE'LS SOLD ON'S MOR PRAIN HAWA-MERVE SPOWTH FACTION PREC	- <u>15</u>	3.16 3.16
g1:14:0.3.8 ref MF 044935.1 nypothetical protein MP 044931	13	5.16
gio6 + p. 4 pir HisETisA nerve growth factor beta chain precurs gio14 / 173.8 ref MF 044985.1 hypothetical protein MP 044986 gio15 gio15 ref MF 4759.1 hypothetical protein SIIP (rp gio16 ref MF 4759.1 hypothetical protein SIIP (rp gio17 ref MF 4759.1 hypothetical protein SIIP (rp)	<u> </u>	5. 6 4 5 -
gill = 114 fret Nr . = 0100.1		4 55 4 56
gi(1 % 11:4 ref MP [% 61:66.1] 4-metnyl-1 (beta-hydroxyetnyl gi) [MOTOL [75:0.1] Motol homolog protein - sea squirt (gi) 65:63:44. sp. 94:63:4 [BOOL 4-METHYL-1 (B-HYDENMYETHYL gi) [16:1:34:39 ref ME 41:43:3.1	<u> </u>	4 5 ±
$= \frac{\text{gi}(1.341.611) \text{pdb}}{\text{chain}} \frac{1850.8}{\text{chain}} = \frac{\text{Gi}(1.4585858) \text{dh}}{\text{AR6076.09.1}} = \frac{\text{Chain}}{\text{CAY037148}} = \text{chain} \text{chain}$	1.2	1 3 A 1 A A
$\frac{900139913999}{201339913199}$ AARIII.25.1 AARIIII.23 (ECOIIII.3) Similar to be	<u>1</u>	199 199 299
gi 64.5.; pir NGHUBM nerve growth factor beta chain precurs gi 44 gb AAA45954.1 (Ml6613) herve growth factor [Gall gi 5465 pir 548631 nerve growth factor beta chain precurs	$-\frac{1}{1}$	7 - 9 7 - 9
gi[+36] * pin[4A363] nerve growth factor beta chain precurs gi[+34] 4 [gb:AAb36][0.1] (\$610.8) herve growth factor [Mus	1 1 1	7 - 9 7 - 9
gi 11 = 1 = 1 12 2 2 2 3 3 3 3 3 3	1	1 1 1 1 1 1
gi[N11855: pir 156570 beta-herve growth factor - rat (frag gi[45]534] ref NF 0 [49].1] nerve growth factor, peta polyp gi[56417]4[sp]513600 NGF BOVIN BETA-NERVE GROWTH EVCTOR FRE	<u> </u>	753 753
<pre>gip301000E(pdb*186E Y Chain Y, Crystal Structure Of 7s Ngf: gip4083770[sp]P21617 NGF MENLA</pre>	$\frac{-1}{-1}$	Grand Vola
- WALL ALMOUGH FOR ON MOR OBJOY - BROWN ARROYD GROWN FRACTOR PROT	$-\frac{1}{1}$	Timby Timby
gi 116.k 34 ref MP 13113.2 norve growth factor, beta poly gi 0:15.007 mbj BAA 0438.1 (Ab03751:) beta-nerve growth fac	<u>: 1</u> : 1	1 = 15 기급 : 3
gi 176. % 74 ref XP [30103.2] norve growth factor, beta poly gi 0715.07 pbj BAA 0438.1 (AB037517) beta-herve growth fac gi 1641608 ref DP [136106.1] CHORISMATE SYNTHASE [Heliotkac gi 0645103 dbj BAA 04383.1; (AP037513) beta-herve growth fac	<u>1</u>	15 d 15 d
gi 14104991 gb:AAK95325.1 AF351497 1 (AF355457) thaumatin=1 gi 1439187 spiq0907411988 PIG BETA-NEEVE GROWTH FACTOR BEBOU	$\frac{-1}{1}$,÷9 /÷9
gi -dita pir +AP(311 norve growth factor beta chain precurs gi -liflif gb /AAF34114.1 (376:54) truncated beta herve gro	$\frac{1}{1}$	- 4 7 - 4
gi 1.:161/sr P01130 NGF MOUSE BETA-NEFVE GFOWTH FACTOF FREC gi 0130305/pab 1WWW W Chain W, Ngf In Complex With Domain 5	<u>1</u>	7999 769
gi 6815211 abj BAA30440.1; (AB037820) beta-norve growth fac gi 222841 drj BAA3306.1; (200010, beta-nerve growth factor	$\frac{-1}{1}$	iel Val
dilicated piritstidal rerve growth factor beta chair predict.	<u> </u>	789
gi 1342172 pir TM172 perm1 protein - barley fragment;	<u>. 1</u> <u>. 1</u>	753 789
gi +815178 abj+BAA+7437.1 (AB037817) beta-herve growth fac gi +7409503 ab +AAF35780.1 AFU22681 1 (AF222682) beta herve g		789 789
gi 1431715 pdb 1816 A Chain A, Crystal Structure Of Beta Ne gi 0503081 qb AAF17035.1 AF145043 1 (AF145043) beta nerve g	<u>::1</u> ::1	789 789
<pre>gi 57696% pdb 1BET</pre>	<u>.:1</u> <u>.:1</u>	763 763
$\frac{gi 7237666 gb AAF5131s.1}{gi 15735154 ref MF 185106.1} = (AE003625) Sps2 gene product [Cro gi 15735154 ref MF 185106.1] truncated pilin [Meisseria men]$	<u>::1</u>	14 5 ± 14 5 ±
<u>gi 1381038 gb AAB9.748.1 </u> (US8844) pilin [Neisseria gonornn <u>gi 2301981 gb AAG38439.1 </u> (AB049646) pilus subunit [Neisser	<u>::1</u> ::1	1055 1055
<pre>gi 1387.705(emb CACOT626.1)</pre>	- <u>.:1</u> -:1	1:0:= 1:0:=
- gil 23210611 gb/AAC $3+435.11$ $-$.APC 476517 rilus subunit (Neisser	- <u>:1</u> - <u>:1</u>	1/18 4 1/18 4
gi 1:F04007 gb AAE 1755.1:AAE01768 BC 01755 hypothetical gi 1:8:1761 gb AAE01749.1	<u> </u>	1 () () () 1 () ()
- qili: Godmalophaab'baya.iAri qubbi i - Arbustus reverse tra		100 :
gi:1: 73:1:8 ref NP N:3110.1 truncated pilin [Neisseria men gi:1:81701/gb:AAB01767.1: U58843) pilin [Neisseria gonorrh gi 46041] gb AAA31313.1: (N.3833) pilin [Neisseria gonorrho	<u> 21</u>	1:3-
gi 2921601: gb:AAC36437.1: (AFc47651) pilus subunit [Neisser	$\frac{21}{21}$	14.58

```
qi|1081693|qb|AAB02745.1|
                                                                                                                                              (U58°41) pilin [Neisseria genorrh...
                                                                                                                                                                                                                                                                                                                                                            1058
                                                                                                                                                                                                                                                                                                                                                                                            1 4 8
                                                                                                                                               (AF0)2040) heta-1,4-xylosidase [L...
   qi:4416191|gk:AA14:24:.1:
   gi 4.64 + gb/AAA. [vi2.1] (L28 ++0) pilin (Neisseria gonorrho...
                                                                                                                                                                                                                                                                                                                                                                                                 1 0.3
   gi|4::41::ab|AAA-4463.1| (L289 % pilin [Neisseria genorrho...
                                                                                                                                                                                                                                                                                                                                                                                               1 11 2
   qillbel": 7 qb (AAkol764.1) | Wisherl pilin [Neisseria acherrh...
                                                                                                                                                                                                                                                                                                                                                                                          1 4 8
1 4 8
  di | 1040°1 pir | 31000 nerve growth factor - monocled ockra ...
di | 2810.50 gb | AA800118.1 | AF179055 1 (AF279053) selenuphosph...
di | 400410 gb | AAA. 1010.1 | Ma8441 pil.n [Meisseria ginorrho...
  qi: [1.-10...ap|P21:77 NOF NAJAT NEFVE GROWTH FACTOR (NGF)
qi: [1.-10...ap|P21:77 NOF NAJAT NEFVE GROWTH FACTOR (NGF)
qi: [1.-16.0...ab|AAROC744.1] (US8840) pilin [Neisseria donorrh...
qi: 40.7765: sp[P34:18 NOF BUNNO NESVE GROWTH FACTOR PRECUESOR...
qi: [1...ap|P34:18 NoF Bunno NESVE GROWTH FACTOR PRECUESOR...
qi: [1...ap|P34:18 NoF Bunno NESVE GROWTH FACTOR PRECUESOR...
| General Content | General Co
                                                                                                                                                                                                                                                                                                                                                                                         1 1 :
                                                                                                                                                                                                                                                                                                                                                                                      1.58
1088
1188
1086
1086
                                                                                                                                                                                                                                                                                                                                                                                                1053
                                                                                                                                                                                                                                                                                                                                                                                      14.0
14.0
                                                                                                                                                                                                                                                                                                                                                                                              14.0
```

Alignments

```
Score = 23.5 bits (4\pi), Expect = 181
Identities = 7/8 (87%), Positives = 7/8 (87%)
Query: 1 CATDIKSA 8
        CATEL GA
Sbjot: 3 CATEGISA 3
\frac{\cdot \text{gi}(14)30474 \mid \text{emb}(7AC4)518.1)}{\text{Dength} = 1067} \text{ (A.5314790) putative zinc finger protein [Homo sapiens]}
Score = 20.7 bits (4\pi), Expect = -326
Identifies = 6.7 (89.), Positives = 6.7 (85)
Query: ∹
          DIRGAET 19
          DIEG ET
Sbjot: 49/ DIKGTED 603
-gi 432303 - gb(AA)10416.11 AF1 (.058) :uter surface protein C precursor (Burrelia sp
         Length = .11
Score = 21.7 b.ts (40), Expect = (52)
Identities = 7/8 (57%), Positives = 7.8 (87%)
```

```
@uery: 2 ATDIKGAE →
                              Date.
           ATE KGAE
Sbjet: 164 ATLTKGAE 171
egi/128165|sp|P.0675 NGF PRANA BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF) Length = 241
 Score = 11.7 bits (46), Expect = -326
 Identities = 7/8 (\% ), Positives = 7/8 (37\%)
Çriery: .
           ATTIKGAE +
           ATEING E
Skjet: 143 ATTINGME 186
gi[63054:pir][MGRTBA nerve growth factor beta chain precursor - multimammate rat
            (Mastomys natalensis)
           ch[AAA408.0.1] (M22743) nerve growth factor [Mastomys natalensis]
           Nemath = 303
 Score = 22.7 bits (46), Expect =
 Identities = 7.8 (878), Positives = 7.8 (878)
          ATE INGAE 3
Query: I
           ATDIKG E
Sbjet: L11 ATDIKGNE L18
rgi(14772379|ref(MP 044985.1| hypothetical protein XP_044985 [Homo sapiens]
          Length = 603
 Score \approx 33.7 bits (46), Expect \approx
                                     32.6
 Identities = 6/7 (85%), Positives = 6/7 (85%)
Query: 4 DIMGAEC 1:
           DIFF ED
Sbjet: 819 DIFFEED 5.8
>gi|15668365|ref(MP .47159.1| SSU ribosomal protein S11P (rpsK) [Methanococcus janna
 qi|17107.5|sr|P54021 RS11 METJA 30S FIBOSOMAL PROTEIN S11P
 <u>gi|:11905.|pir |864813 ribosomal protein 811 - Methanococcus jannaschii</u>
gi|1890936|gb+AAB98171.1| (U67475) SSU ribosomal protein 811P (rpsK) [Methanococcus
           mannaschii)
           Length = 119
 Score = 22.7 bits (46), Expect = -326
 Identities = 7/8 (87%), Positives = 7/8 (87%)
Query: I ATDIKJAE 9
          ATDI GAE
Sbjet: 25 ATDITGAE 32
sgi|16123334<u>{re:|NP-406647.1|</u> 4-methyl-E(B-hydroxyethyl)-thiazol monophosphate biosy
          enzyme [Yersinia pestis]
 gi|159%1111 em: |CAC40407.11 (AJ41415) + 4-methyl-5(B-hydroxyethyl)-thiazol monophosp
          biosynthesis enzyme [Yersin.a pestis]
          Hergin = 136
 Score = 20.3 \text{ bits } (45), Expect = -408
 Identities = 6.6 (1.0\%), Positives = 6/6 (100\%)
           IKGAET 10
Query: 1
                             Date
           KGAE :
Sbjet: 76 IKGAE® 61
eqi:158001:4:ref:MP 286166.1: 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate s
```

```
[Escherichia ocli 0157:H7 EDL933]
 gi 15829732 ref(NP 308505.1 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate s
'Escherichia coli 0157:H7]
 synthesis [Escherichia coli 0157:H% EDL933]
 gi|13389486|Bhj|3AB53901.1] (AP902551, 4-metnyl-5(beta-hydroxyethyl)-thiazole monop
         synthesis [Escherichia coli (157:H7]
          Length = 198
 Score = 22.3 k:ts (45 , Expect = - 43-
 Identities = 6/6 (1998), Positives = 1/6 (1998)
Query: [
        IKGAED 11
          IKGAEC
                        . . . . . .
Sbjot: 78 IKGAEC 83
>gi|7522619 pirt:T52201 Notch homolog protein - sea squirt (Halocynthia roretzi)
 gi|304+867 dbj BAAJ:571.1| (ABCU1327) HrNotch protein [Halocynthia roretzi]
Length = 2352
 Score = 11.3 bits (48), Expect = 438
 Identifies = 7/10 / (700), Positives = 7/10 (700), Gaps = 2/10 (200)
Query: I
          CATIIKGAEC 10
CATOI EC
Sbjet: 791 CATOIN--EC 798
>gi|668+641|sp_Q46948|THII ECOLI 4-METHYL-5(B-HYDROXYETHYL)-THIAZOLE MONOPHUSPHATE B
ENZYME
         Length = 196
 Score = 22.3 bits (4t), Expect = 438
 Identifies = 676 (1995), Pisitives = 676 (1993)
Query: % INCARC 10
          IMGAE
Sbjot: 76 INGAED 81
bicsynthesis protein [Escherichia coli]
gi[17806]6|gb[AAC73827.1] (AE000148: 4-nethyl-5(beta-hydroxyethyl)-thiazole monopho
          synthesis (Escherichia coli KL)
          Length = 138
Score = 22.3 bits (45), Expect \approx 435
 Identities = 6.5 (100%), Positives = 6.5 (100%)
Query: 5
         IKGAEC 10
                      \mathcal{O}_{k} , \mathcal{O}_{k}
          IKGAEC
Sbjet: 78 IKGAEC 83
egif1942612fpdk 1HEO B Chain B, Molecular Structure Of A High Potential Cytechrome C
          Isolated From Phodopila Globiformis
 gi:1342611:pdb 1HRO A Chain A, Molecular Structure Of A High Potential Cytochrome C
          Isolated From Phodopila Globiformis
          Length = 106
Score = 32.3 \text{ bits } (45), Expect = 438
 Identities = 7.3 (87\%), Positives = 7/8 (87\%)
Query: 1 CATDINGA 8
```

```
C TEIMGA
Sbjot: 02 CHTEIMGA 39
 -gi[14585855]gb AAK67629.1] (AY037148) phosphatidylethanolamine binding protein [Hom
                     Length = .1.7
 Score = 31.8 kits = 44; Expect = 588
 Identifies = 6.7 \text{ (MBL, Positives} = 7.7 \text{ (39%)}
Query: 3 TEHKGAE &
                       T'E I KGA+
Sbjet: 110 TEIKGAD 182
Mai|1501.4803|dr AAH11123.1(AAH11123 (BCC11123) Similar to herve growth factor, beta
                      Length = 134
 Score = 0.1.4 hits (42), Expect = 0.78 h
 Identifies = 7/8 (e<sup>7</sup>), Fositives = 7/8 (87%)
Query: 1 AIDIKGAE 3
                       ATDIKG E
Sbjot: 215 ATBIRGKE 7.02
egi[7305313]ref NF 03<u>5637.17</u> nerve growth factor, beta [Mus musculus]
  gi|69053 pir||NGMSMG nerve growth factor beta chain precursor - mouse
  gi[1:1365 emb[CAA247.11.1] (V00936) precursor of NGF [Mus musculus]
  gi|200054|gb|AAA398_1.1| (M.4805) nerve growth factor beta [Mus musculus]
 | Column | C
  gi|357171|qb|AAA376%6.1| (M17398) nerve growth factor [Mus musculus]
  Score = 21.4 buts (41), Expect = -78 \times
 Identities = 7/6 (6/4), Positives = 7/6 (676)
Query: P ATBIKGAE 9
                        ATEUKS E
Sbjot: 015 ATDINGKE 012
>di[6308] pir[(NGHUBM nerve growth factor beta chain predursor - human (fragment)
 gi[[23090]prf] [300237A nerve growth factor beta [Homo sapiens]
Length = 200
  Scare = 21.4 buts (48), Expect = -783
  Identities = 7/3 (8%), Positives = 7/3 (8%)
                       ATEHKSAE #
Query: ∟
                        ATDIKG E
Sbjet: 194 ATDINGKE 331
 -gi(11244 | gb(177A484)4.1| (M26810) nerve growth factor [Gallus gallus]
                      Lengt: = 1. :
 Spane = 21.4 bits (43), Expect = 78)
 Identifies = 7.8 \text{ (cl.)}, Positives = 7.8 \text{ (87%)}
Query: D ATDIKGAE B
                      ATDIES E
Skijot: 32 ATDIKGRE 3+
 	imes q i (3467) pin: A2631, herve growth factor beta chain precursor - bovine (fragment)
 ci 163410 gb AAA30666.1 (M26809) nerve growth factor [Bos taurus]
                      Length = 1.1
```

```
Score = 21.4 \text{ hits } (43), \text{ Expect} = 789
 Identities = 7/8 (°7), Positives 7/8 (87)
Query: 2 ATDINGAE :
           ATDIE: E
objet: 33 ATDIKSKE 40
-91[A248742] db[AAB268, 0.2] -862089) nerve growth factor [Mus sp.]
            Ler.at:. = . 71
 Score = 0.1.4 kats 0.40), Expedt = 0.784
 Identities = 7.8 (47.4, Positives = 7.8 (878)
           ATDIKSAE 3
Query: 3
             ATDIKG E
Sbjot: 149 ATDINGKE 156
>qi[/11=653|pir:|156570 beta-nerve growth factor - rat (fragment)
 gij. 05630 gb(AAA41030.1) (M36583) beta-nerve growth factor [Rattus norvegicus]
            Length = L3%
 Score = (1.4 \text{ kits } (4)), Expect = (769)
 Identities = 7/8 (87%), Positives = 7/8 (87%)
Query: 2 ATMIKGAE 3
             ATEING E
Sbjet: 183 ATDINGKE 160
egi(400):391(ref MF 00:497.1 merve growth factor, beta polypeptide; Nerve growth fac
             [Home sapiens]
gi|128161|sp|E01138.NGF HUMAN BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
gi|19477 emb|CAA36830.1| (M38899) beta nerve growth factor (AA 1-241) [Homo sapiens
gi|19903|gb|AA449031.1| (M21062) nerve growth factor beta [Homo sapiens]
gi|67198|(emb|CAA24735.1) (V01911) beta-nerve growth factor [Homo sapiens]
Length = L91
 Score = 21.4 bits (45., Expect = -784)
Identities = 7/8 (87., Positives = 7/8 (878)
Query: 1
             ATEIKGAE 9
             ATDIKS E
Shipot: 149 ATELEGRE 156
Sgif3(417.4)spff13600 NGF BOVIN BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
 cittl8-7:0|emb CAA70059.1| (Y09566) beta-nerve growth factor [Bas taurus]
           Length = 231
 Score = 21.4 \text{ b:ts } (43), \text{ Expect} = 783
 Identities = 7.6 (87%), Positives = 7.8 (87%)
Query: .: ATDINGAE 9
             ATDIKG E
Sbjot: 139 ATDINGKE 146
hgi[H31.608]pdk 1SGFTY Chair Y, Crystal Structure Of 7s Ngf: A Complex Of Nerve Grow
            Factor With Four Binding Proteins (Serine Proteinases)
 gif3211615|pdk 18GF/B Chain B, Crystal Structure Of 7s Ngf: A Complex Of Nerve Grow
            Factor With Four Binding Proteins (Serine Proteinases)
            Length = 115
 Score = .1.4 buts .43, Expect = .78?
 Identifies = 7/8 (87%), Positives = 7/8 (87%)
Query: 2 ATDIKGAE 3
```

```
ATDIKG E
Sbjct: 28 ATDIKGKE 35
-ai:403-770/sp:21617:NGF MENLA NERVE GROWTH FACTOR PRECURSOR (NGF)
            Length = .:31
 Score = 21.4 \text{ bits } (43), Expect = -789
 Identities = 7/3 (\pm 7/3), Positives = 7/8 (87\%)
query: 1 ATDINGAE 3
            ATDING E
Ubjet: 141 ATCHRONE 143
-gi[155.445]sp[F254.77]NGF RAT BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
            Length = 141
 Score = 21.4 kits [43], Expect = -78\pi
 Identities = 7/8 (87%), Positives = 7/8 (87%)
Query: I ATOIKGAE 9
            ATDING E
Object: 14% ATDIKSKE 186
hgi|128160|sp|E05000 NGF CHICK BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
            Length = 143
 Score = 21.4 \text{ kits } (43), Expect = 789
 Identities = 7/3 (871), Positives = 7/8 + 671)
Query: 1 ATDIESAE 9
            ATDING E
Sbjot: 150 ATDIKGKE 189
\frac{\text{cgi}[13676.74]\text{ref}[XP]002122.2)}{\text{gi}[13676.74]\text{ref}[XP]002122.2)} \text{ nerve growth factor, beta polypeptide [Homo sapiens]} \\ \frac{\text{gi}[13676.74]\text{ref}[XP]002122.2)}{\text{gi}[39776.95]\text{gb}[AA..53.375.1]AFI50960]} \text{ (AFI50960) nerve growth factor B [Homo sapiens]}
 gi[7018-000 temb-CAB78-625.1] (AL049825) dJ662B22.1 (nerve growth factor, beta polypep
             sariens]
           Length = 241
 Score = 11.4 bits (43), Expect = -78?
Identities = 7/8 (57%), Positives = 7/8 (37%)
            ATDINGAE 9
Query: I
             ATDIEG E
Objet: 149 ATDINGHE 156
-gi(6815237 dbj BAA96438.1 (AB037518) beta-nerve growth factor [Pan troglodytes]
            Length = 241
 Score = 11.4 bits (48), Expect = -788
 Identities = 7/8 (87%), Positives = 7/8 (37%)
          ATTIFGAE 9
Query:
             ATCIFG E
Ubjet: 149 ATCINGKE 136
*gi+15611-75\ref!NP 223326.1! CHORISMATE SYNTHASE [Helicobacter pylori J99]
 gill11314481sp QHZLH1 AROC HELPJ CHORISMATE SYNTHASE (5-ENGLPYRUVYLSHIKIMATE-3-PHOS
             PHOSPHOLYASE)
 gi[743~253!pir![F7191] chorismate synthase - Helicobacter pylori (strain J99)
 gi[4155160]gb[AAD06189.1] (AE001492) CHORISMATE SYNTHASE [Helicobacter pylori J99]
 Score = 21.4 \text{ bits } (43), Expect = 782
```

```
Identities = 6.7 (85), Positives = 6.7 (85)
         DIKGAEC 1 -
Query: 4
          DIKG EC
Objet: 30% DIKGNEC 315
-gi[-08152]9|dkj BAA+1439.11 (AB037519) beta-nerve growth factor [Gorilla gorilla]
          Length = .341
 Score = .1.4 bits (47), Expect = -78)
Identities = 7/8 (**), Positives = 7/6 (87%)
        ATE I HOAE
Query: I
          ATCIEG E
Sbjot: 144 ATEINGKE 186
-di|14164981|qb|AAK55725.1|AF355457 1 (AF355457) thaumatin-like protein TLP7 [Hordeu
         Length = 1.7
 Score = 11.4 bits (43), Expect = 780
 Identities = 8/11 (7.%), Positives = 8/11 (72%), Gaps = 3/11 (27%)
         CATEL-KGAEC 10
Query: 1
          CATDI K EC
Sbjot: 145 CATDITK--EC 153
>gi|1499157|sr+q29074 NGF PIG BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
 gi|533771|gb|AAA.1501.1| (L31898) nerve growth factor B [Sus scrofa]
          Lenath = ....
 Score = 21.4 kits (4:), Expect = -78!
 Identities = 7.8 (-7), Positives = 7.8 (878)
Query: ...
         ATPIKSAE 🧎
          ATDIKS E
Sbjot: 137 ATTIKSKE 144
-gi[86383[pir][A2631] nerve growth factor beta chain precursor - chicken (fragment)
 gi|1334740|emb+CAA.7633.1 (X04003) prepro-polypeptide (aa -123 to 118); gtg start
          gallus]
         Length = 140
 Score = 21.4 bits (45), Expect = -783
 Identities = 7.8 (67); Positives = 7.8 (67)
          ATDIKGAE 9
query: 2
          ATDING E
Sbjot: 15/ ATDINGKE 199
gi|8157159|qb|AAB34114.2| (S76884) truncated beta nerve growth factor; beta-NGF [Ho
          sariers]
          Length == -7
 Score = 11.4 bits (45), Expect = 1
 Identities = 7.8 (+7), Positives = 7.8 (87*)
Query: 2 ATMIFGAE 4
         ATE/IEG E
Sbjot: 28 ATEIKGKE 👊
-gill28161(splf)1130(MGF MOUSE BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
         Length = 1:4:
 Score = 1.4 bits (4a), Expect = 780
```

```
Identities = 7/8 (87%), Positives - 7/8 (87%)
Query: 2 ATDIYGAE 9
                         ATDIEG E
Ubjet: 149 ATDINGME 156
 odil: 1375-5 pob: 1888 W Chain W, Nof In Complex With Domain 5 Of The Trka Receptor
  gile1375.4 pak 1WWW 7 Chain V, Ngf In Complex With Domain 5 Cf The Trka Receptor
  gi [ ])84 年 [gb] [AVA728(0.1) (M30504) nerve growth factor [synthetic construct]
                       Length = 12
  Score = 11.4 kats -41, Expect = -789
  Identities = 7.8 \times 7 , Positives = 7/8 \times 1878
Query: 2 ATTIKGAE 2
                       ATDING E
Sbjet: 18 ATDINGME 35
ogiju815001 | drj (874.20440.1) (AB037520) beta-nerve growth factor [Pongo pygmaeus]
                       Length = .41
  Score = 21.4 bits (45), Expect = 785
  Identities = 7/8 (87); Positives = 7/8 (87%)
                        ATCIFGAE 4
Query: 🗈
                          ATDING E
Sbjot: 149 ATDINGKE 116
 \frac{(\text{gi}) \cdot 21 + 41 | \text{dbj}) \mid \text{FAA} \mid 00008.1}{\text{gi} \mid 055 \mid 54 \mid \text{embj} \mid \text{FAA} \mid 0008.1} \quad \text{(MO4067)} \quad \text{beta-nerve growth factor (aa 1-126) [Gallus factor (ab factor (ab factor (ab factor (beta-nerve growth factor 
                       <u> Lengti = 120</u>
  Score = 11.4 bits (43), Expect = -78x
  Identities = 7/8 (87), Positives = 7/8 (871)
Query: A ATDIEGAE B
                       ATELING E
Sbjet: 35 ATDIKSKE 40
\frac{\text{Sgill})4144[\text{pir}]/\text{S}1448]}{\text{gi}[64915]\text{emb}[\text{CAA3914}],1]} \text{ (X55716) nerve growth factor prepropeptide [Xenopus laevis Length = 13]}
  Score = 21.4 bits +43%, Expect = -78%
  Identities = 7/8 (97 ), Positives = 7/8 (67%)
query: I
                        ATDIKGAE 9
                          ATEING E
Sbjot: 145 ATDIKGKE 152
 -qi|V442172|pir |T04370 perm1 protein - barley (fragment)
  gi||.454602||go||AAE71600.1| (AE016327) | Barperm1 [Hordeum vulgare]
                      Length = 1000
  Score = 11.4 bits (45), Expect = -783
  Identities = 8/11/(72\epsilon), Positives = 8/11/(72\epsilon), Gaps = 3/11/(27\epsilon)
                         CATE I - MGAEC 10
Query: 1
                          CATHI EC
Sbjat: 123 CATDITH--EC 131
 *gi(126159(sp)P19093)NGF CAVPO BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
  gi(33006,pir(3100.97 nerve growth factor beta chain precursor - guinea pig
                       Length = 241
```

```
Score = 31.4 \text{ bits } (43), \text{ Expect} = 789
 Identities = 7.8 (37), Positives = 7.8 (87*)
Query: 2 ATDIKGAE 9
           ATELIEG E
Object: 14 + ATELHGHE 156
-gi[63152]E[dk] BAA90437.1[ (AB)37517) beta-nerve growth factor [Homo sapiens]
           Lengtr = 341
 Score = .11.4 \text{ bits } (43), Expect = .730
Identities = 7.3 (ETB), Positives = 7.6 (87%)
Query: 2 ATDIKGAE 3
            ATMING E
Sbjot: 14 + ATDINGKE 156
eqi|6969508|gb AAF33790.1/AF222652 1 (AF222682) beta nerve growth factor [Macada fus
           Length = 117
 Score = .1.4 \text{ kits} (43), Expect = .78 +
Identities = 7/8 (67\%), Positives = 7/8 (87\%)
Query: 2
         ATDI KGAE (9
            ATDIKG E
Sbjet: 139 ATDINGKE 146
agi|1431718|pdk 1PTG A Chain A, Crystal Structure Of Beta Nerve Growth Factor At 2.5
           Resolution In C2 Space Group With In Ions Bound
 gi|1431776|pdk 1PTG B Chain B, Crystal Structure Of Beta Nerve Growth Factor At 2.5
Resolution In C2 Space Group With On Ions Bound
 gi|1431"17|pak 1ETG C Chair C, Crystal Structure Of Beta Nerve Growth Factor At 2.5
Fessilution In C2 Space Group With Un Ions Bound
           Length = 110
 Scare = 11.4 \text{ kits} (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7.8 (87%)
Query: J ATEMISAE B
           ATDING E
Objet: 30 ATDINGRE 37
#gi1656:X3-2|gb|AAF17935.1|AF145043 1 (AF145043) heta nerve growth factor [Cervus ela
           Length = 87
 Score = 21.4 \text{ bits } (43), Expect = -789
Identities = 7/8 (87%), Positives = 7/8 (87%)
Query: 2 ATTINGAE 9
           ATLING E
Sbjet: 12 ATPINGKE 19
ai!576ur<u>H|pab|1BET</u>
                          Beta-Nerve Growth Factor
           Length = 10^{\circ}
Score = .(1.4 \text{ k:ts} - 43), Expect = ...737
Identitles = 7.8 (474), Positives = 7.8 (878)
Query: D ATBIFGAE +
           ATEING E
Sbjot: 19 ATDIFGKE 16
*gi.1570:313|gb:AAL 5874.1:AF411526 1 (AF411526) nerve growth factor beta [Homo sapi
           Length = 241
```

```
789
 Score = .1.4 bits (43), Expect =
 Identities = 0.78 (87), Positives = 7.8 (87)
Query: 3 ATDIKGAE 9
          ATECHE E
Jbjrt: 149 ATDINGKE 156
Length = 315
 Scare - L1.0 bits (40%, Expect = 105m)
 Identifies = 6.7 (88)., Positives = 6.7 (85)
          CATDING 7
Query: I
          CATDI G
Sbjot: 100 CATDITG 200
Description | 15753184|ref|NP 155108.1| truncated pilin [Neisseria meningitidis Z2491]
 gi|11277072|rir||F82021 truncated p.1.n NMA0266 [imported] - Neisseria meningitidis
         (group A strain 22491)
 gi|/1777019 emk GAB83074.1 (AL162752) truncated pilin [Neisseria meningitidis Z2491
          Lengtr. = 141
 Score \pm 21.0 bits (42), Expect \pm 105:
 Identities = (.6 (100)), Positives = 0/6 (100)
Query: D ATDIKG 7
         ATELLIG
Sbjet: :4 ATSIEG 39
  Database: nr
    Posted date: Oct 23, 2001 6:02 PM
  Number of letters in database: 247,121,334
  Number of sequences in database: 777,663
Lambda
           0.189
   0.356
                     1.88
Gapped
Lambda
          0.110
  0.294
                    0.610
Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Hits to DB: 7,355,637
Number of Sequences: 777663
Number of extensions: 59715
Number of successful extensions: 1516
Number of sequences better than 20000.0: 1509
Number of HSE's better than 20000.0 without gapping: 1509
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1816
length of query: 10
length of database: 247,121,334
offective HSP length: 1
effective length of query: 3
reffective length of database: 246,343,671
effective search space: 2217093039
offective search space used: 2217093033
T: 11
A: 40
X1: 14 ( 7.2 bits)
X2: 35 (14.8 bits)
```

X3: 58 (24.6 bits) S1: 33 (18.7 bits) S2: 33 (17.2 bits)